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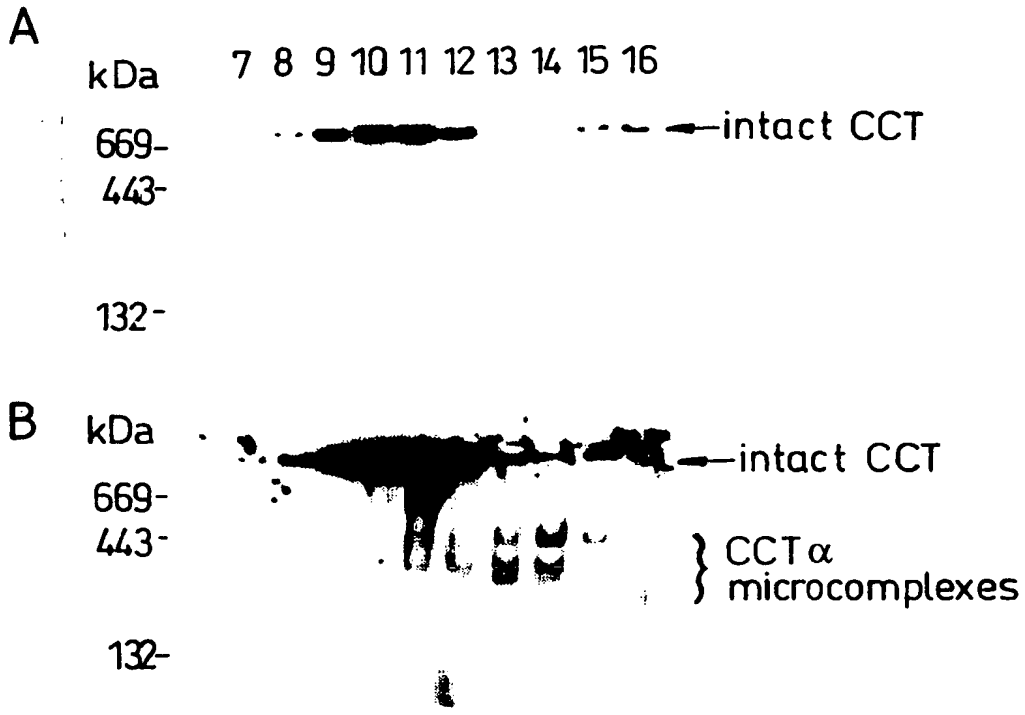


Fig. 1

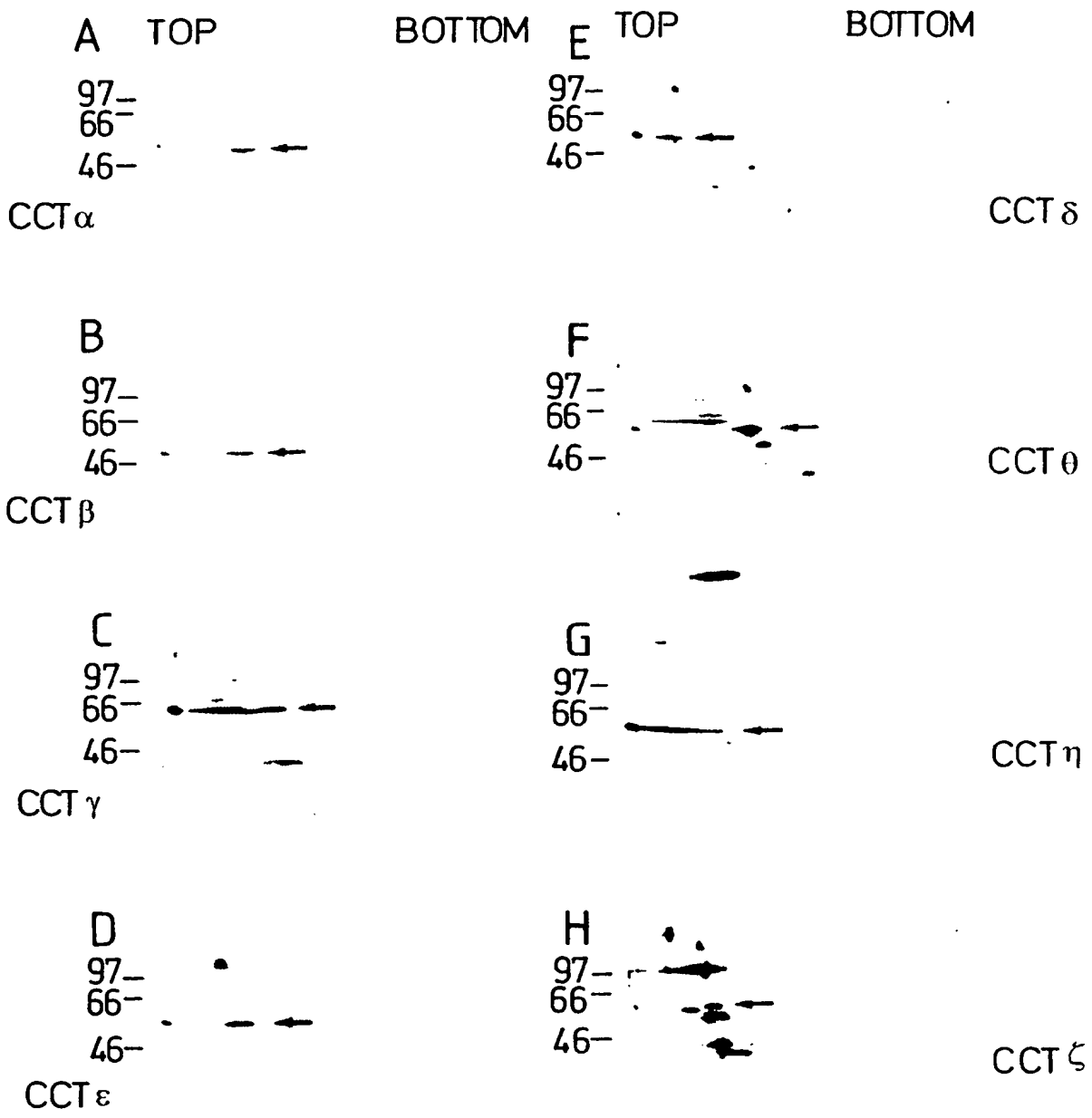


Fig 2

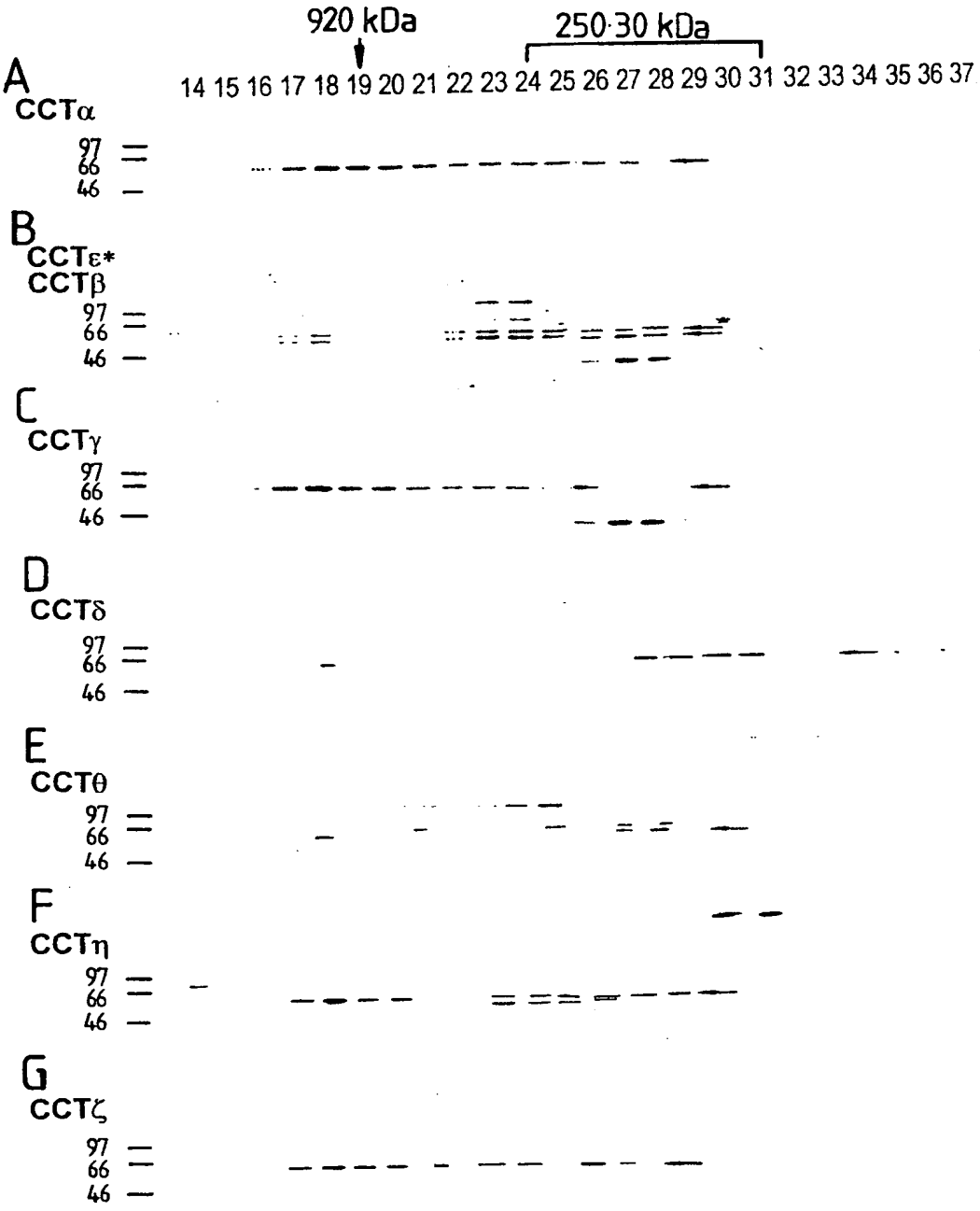
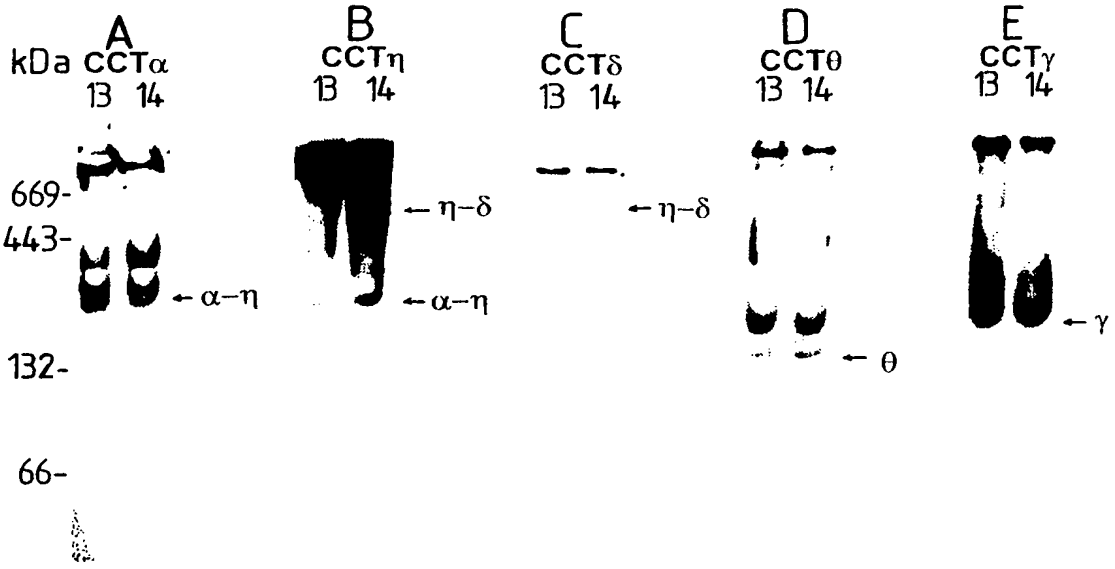
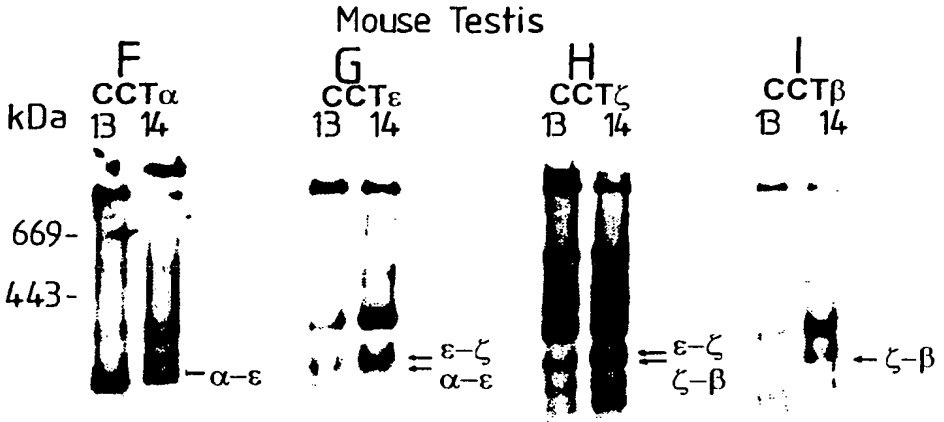


Fig. 3





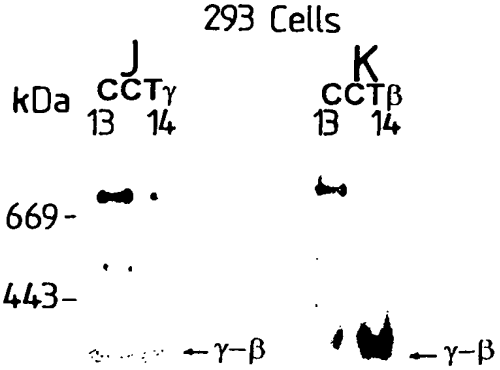


Fig 4

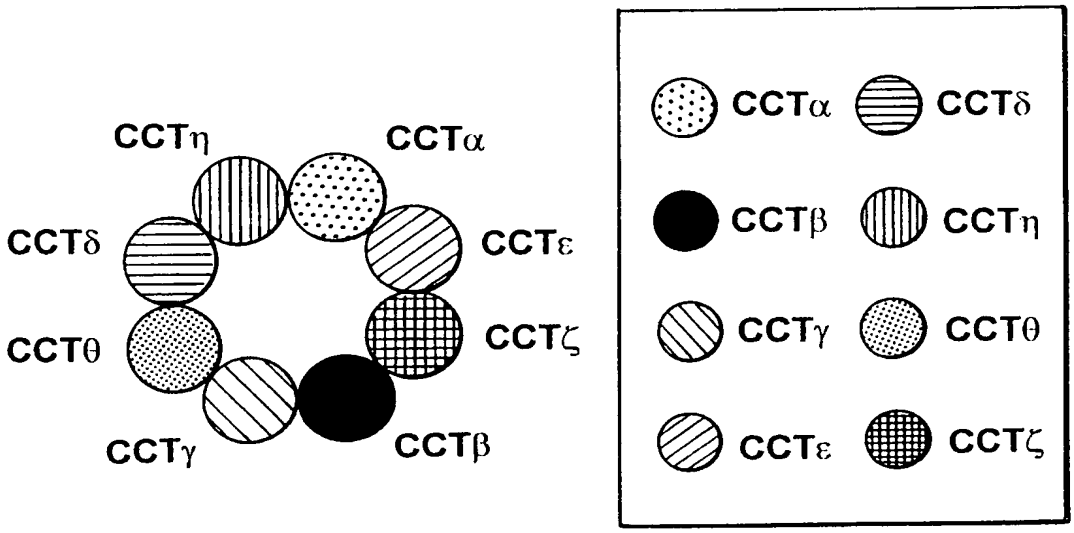


Fig. 5

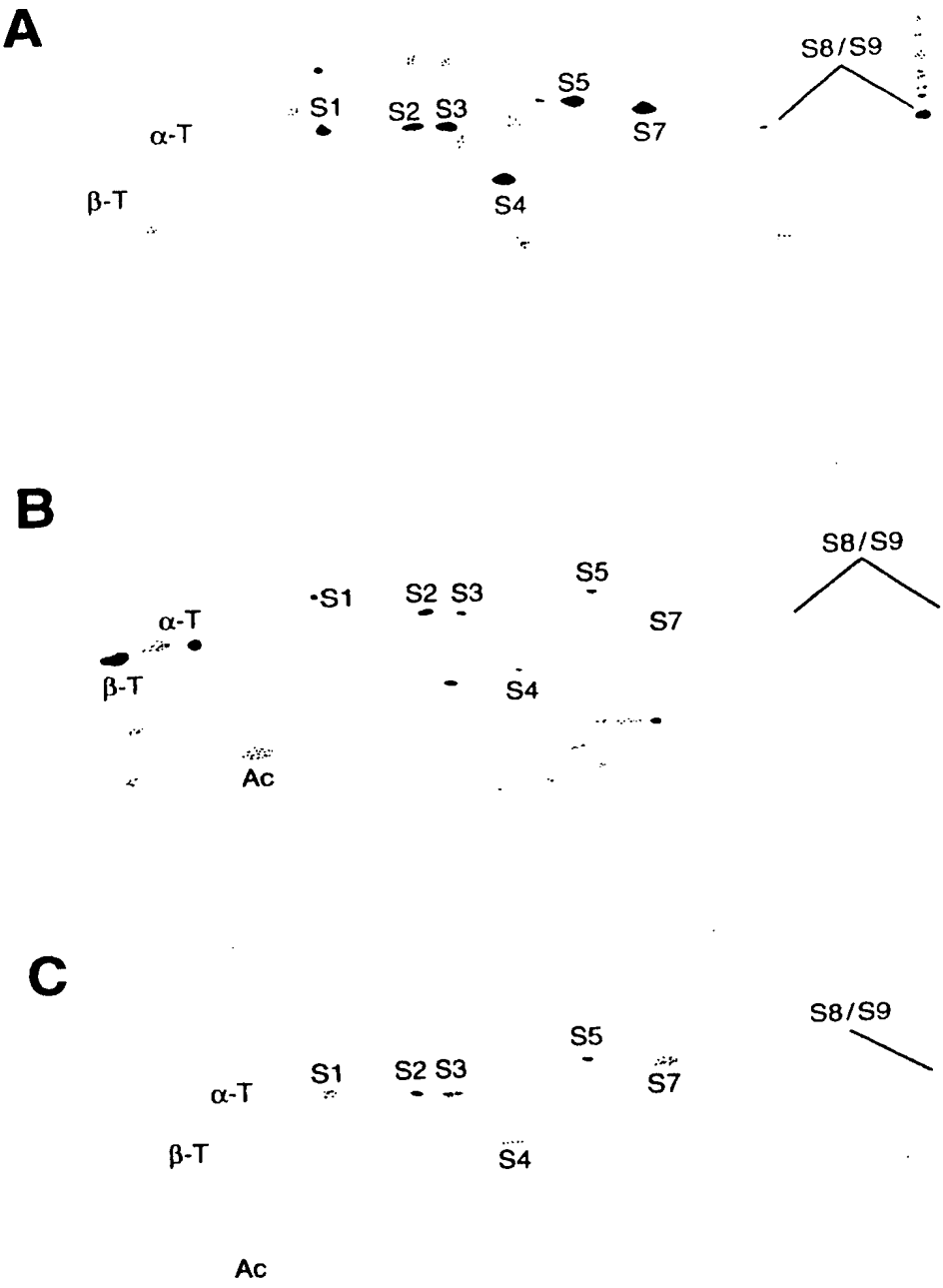


Fig 6

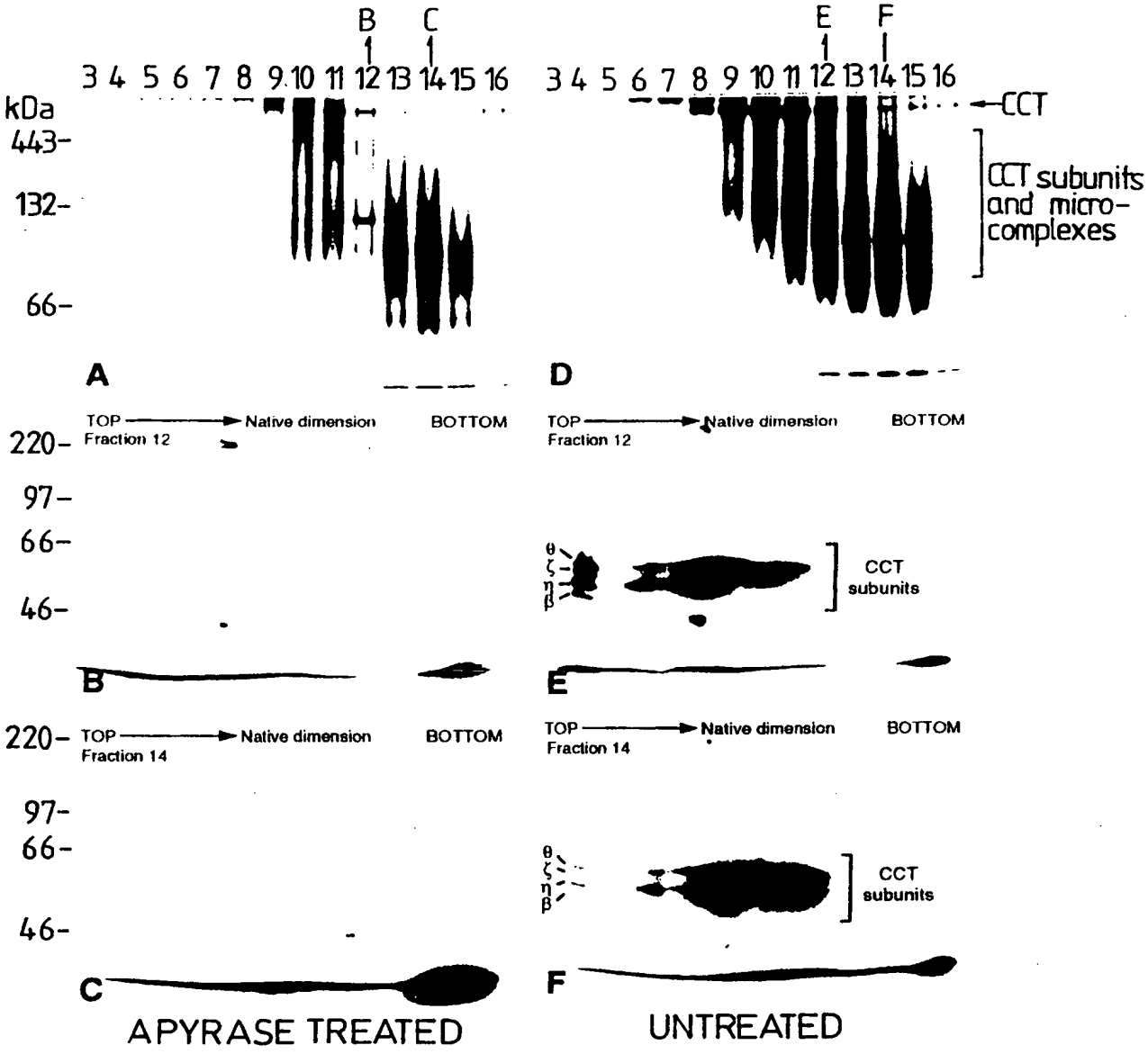
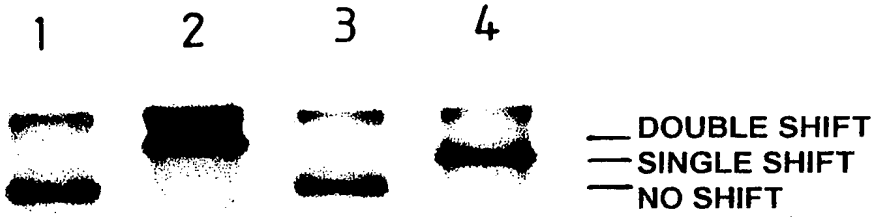


Fig. 7

A

	555	
Rabbit CCTα	...AVHSGAL	D D
Mouse CCTα	...AVHSGAL	D D
Mutant	...AVHSGAL	N D

B



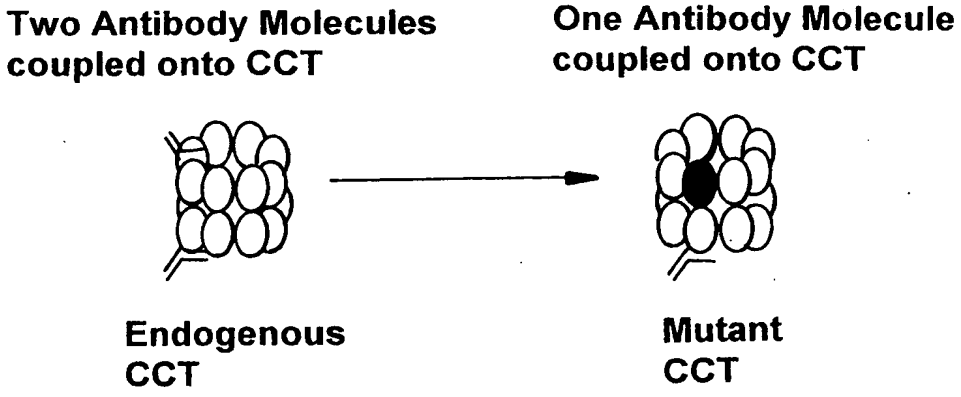


Fig 8

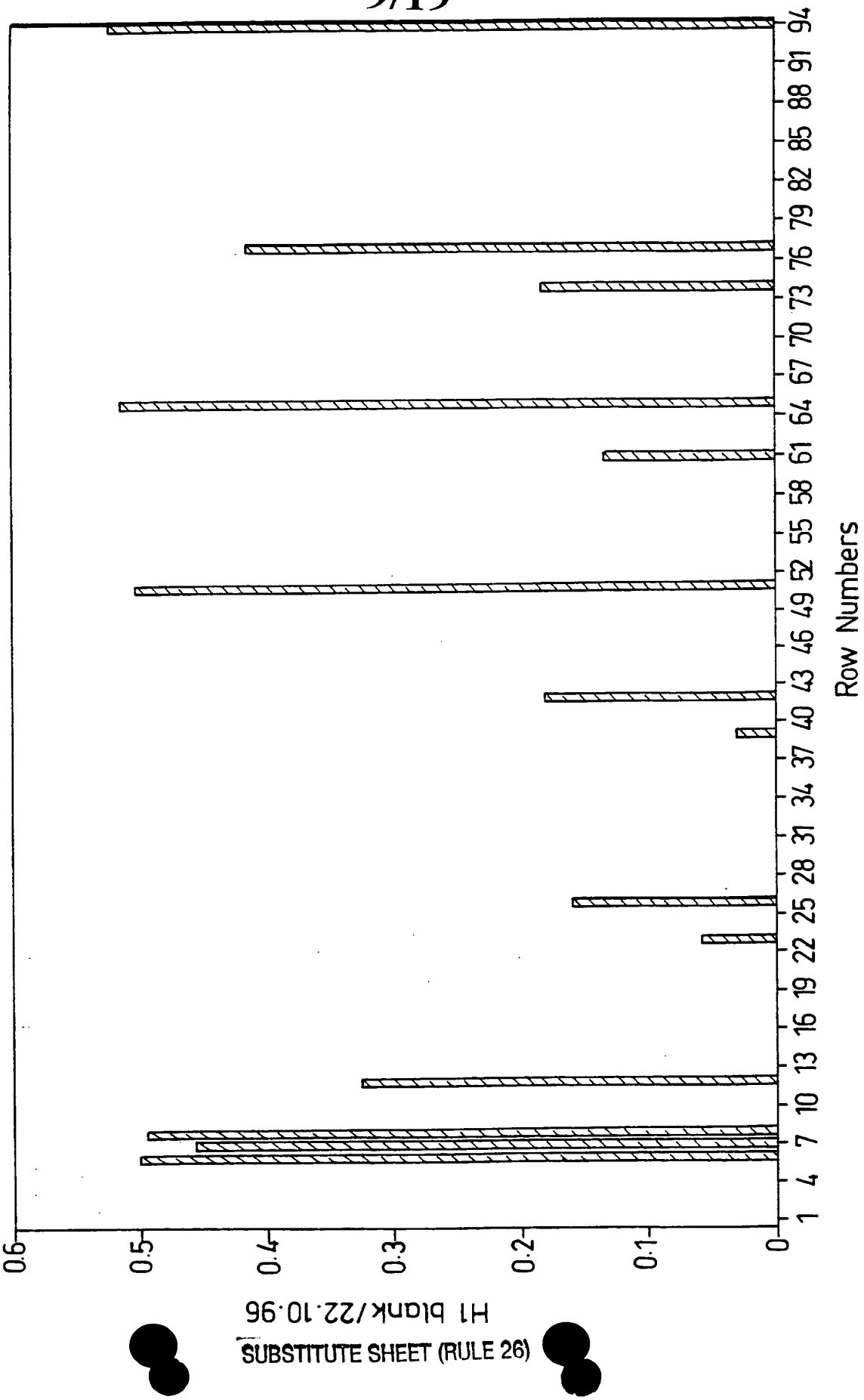


Fig. 9

Fig 10

Peptide Sequences

Reference Peptide No.	Peptide No. In Figure 11	Peptide Sequence
1	6	APRAVFPSIVGRPRH
2	7	FPSIVGRPRHQGVMV
3	8	GRPRHQGVMVGMGQK
4	61	GGTTMYPGIADRMQK
5	77	PRHQGVMVGMGQKDS
6	26	TFNTPAMYVAIQAVL
7	35	LPHAILRLDLAGRDL
8	70	LASLSTFQQMWISKQ
9	12	DEAQSKRGILTLKYP
10	28	IQAVLSLYASGRTTG
11	39	KILTERGYSFTTTAE
12	40	RGYSFTTTAEREIVR
13	47	ASSSSLEKSYELPDG
14	65	APSTMKIKIIAPPER
15	67	APPERKYSVWIGGSI

Lane 1 Peptide 8 at 13.3 μM	(Biotin-SGSGGRPRHQGVMVGMGQK)
Lane 2 Peptide 8 at 1.33 μM	(Biotin-SGSGGRPRHQGVMVGMGQK)
Lane 3 Peptide 8.1 at 13.3 μM	(Biotin-SGSGARPRHQGVMVGMGQK)
Lane 4 Peptide 8.2 at 13.3 μM	(Biotin-SGSGGAPRHQGVMVGMGQK)
Lane 5 Peptide 8.3 at 13.3 μM	(Biotin-SGSGGRARHQGVMVGMGQK)
Lane 6 Peptide 8.4 at 13.3 μM	(Biotin-SGSGGRPAHQGVMVGMGQK)
Lane 7 Peptide 8.5 at 13.3 μM	(Biotin-SGSGGRPRAQGVMVGMGQK)
Lane 8 Peptide 8.6 at 13.3 μM	(Biotin-SGSGAAAAAQGVMVGMGQK)

Fig. 11a

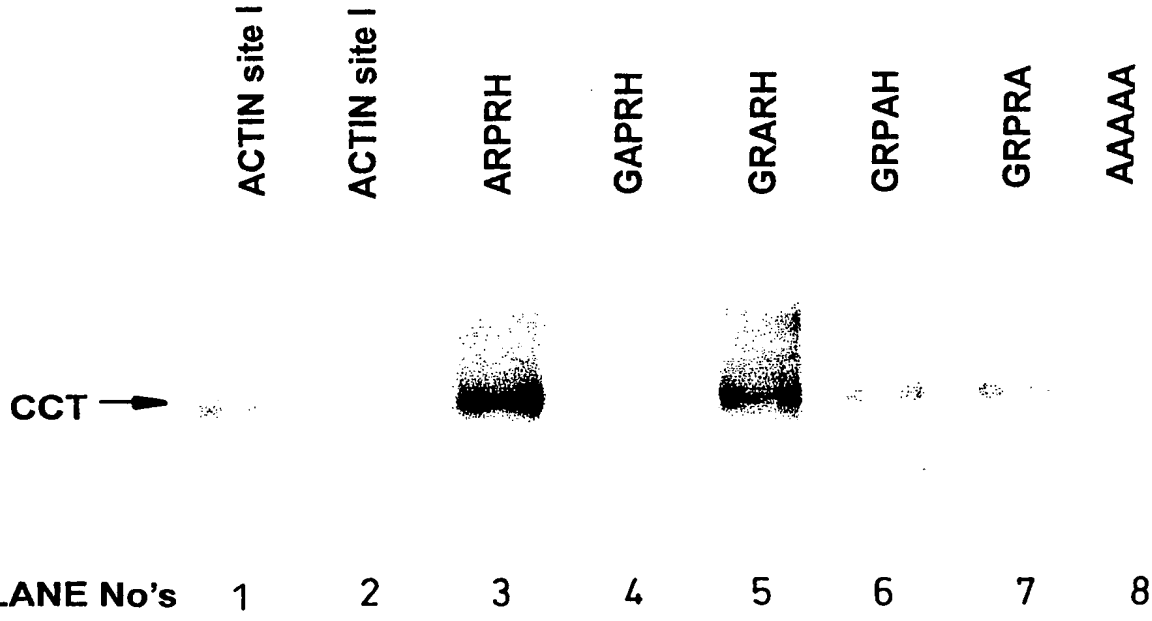


Fig 11b

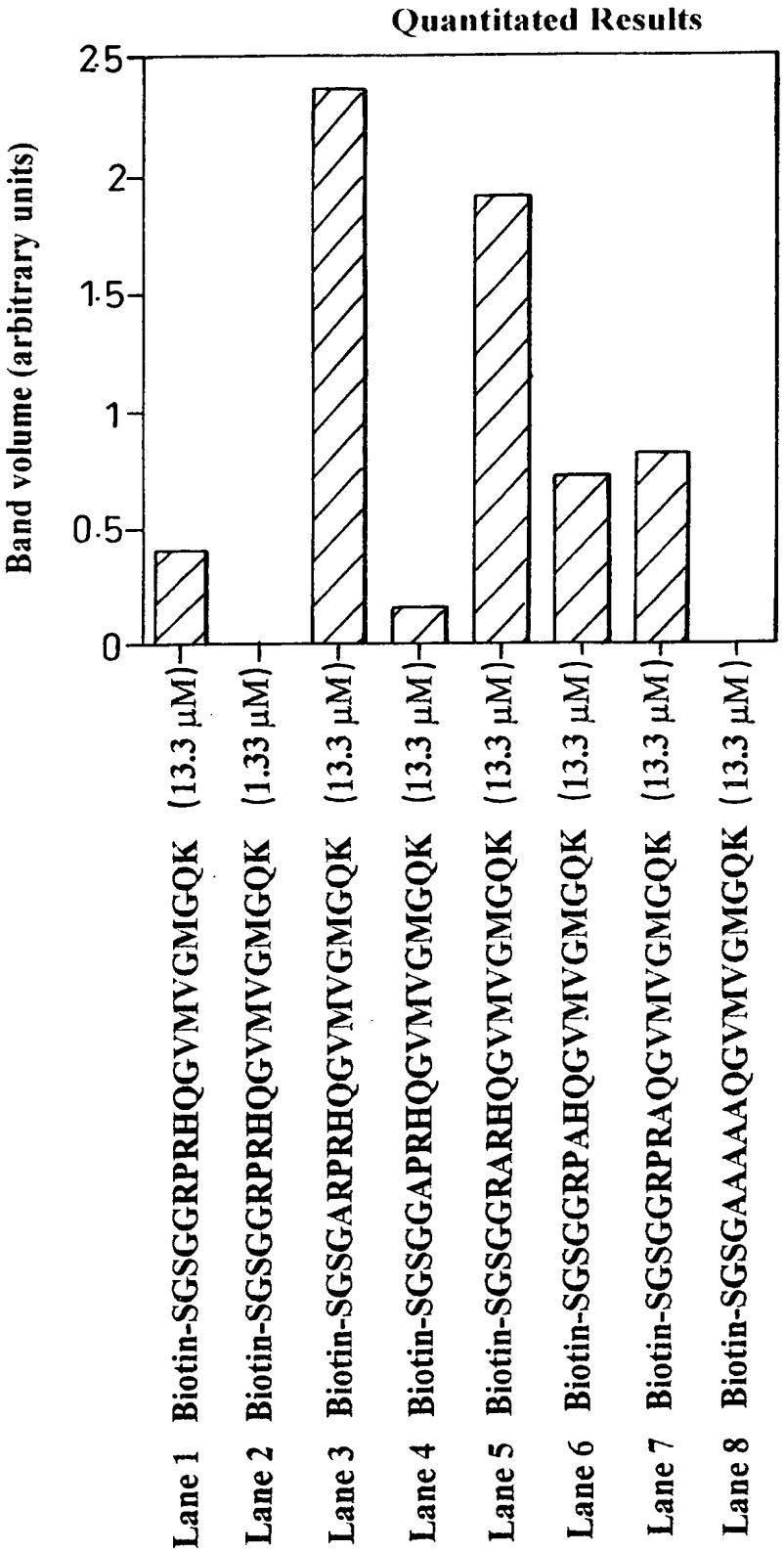


Fig. 11c

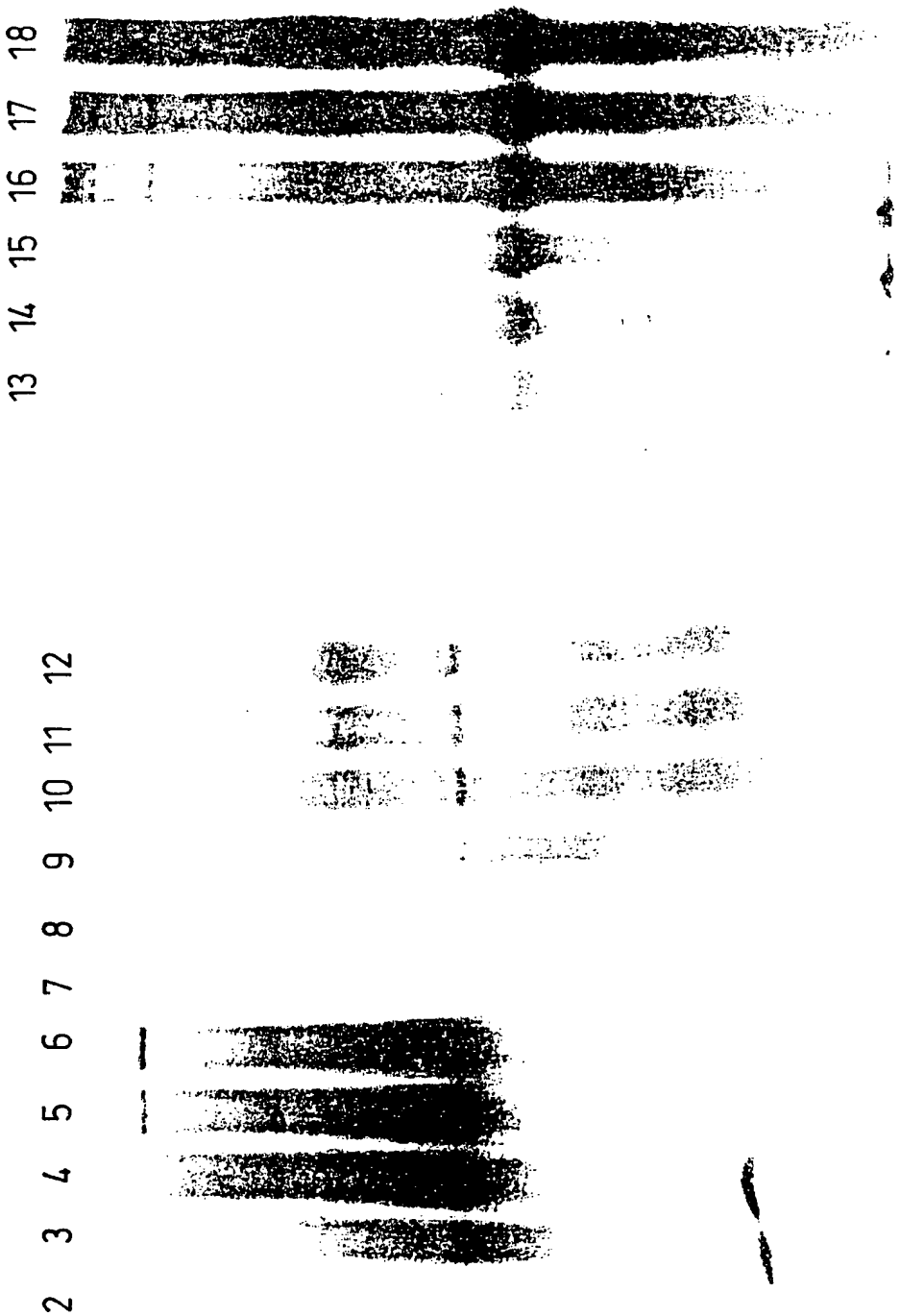


Fig. 12

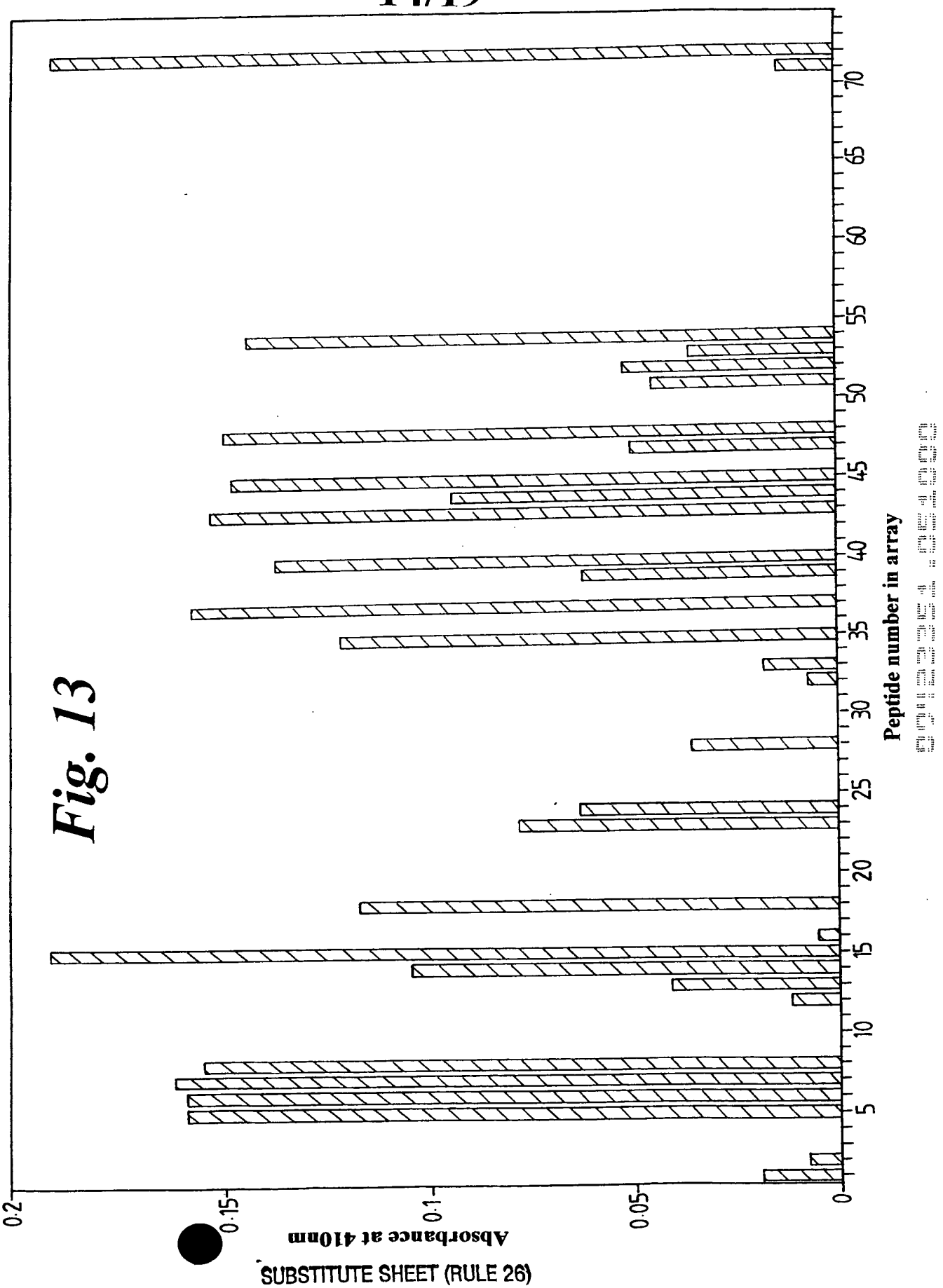


Fig. 13

Fig. 14

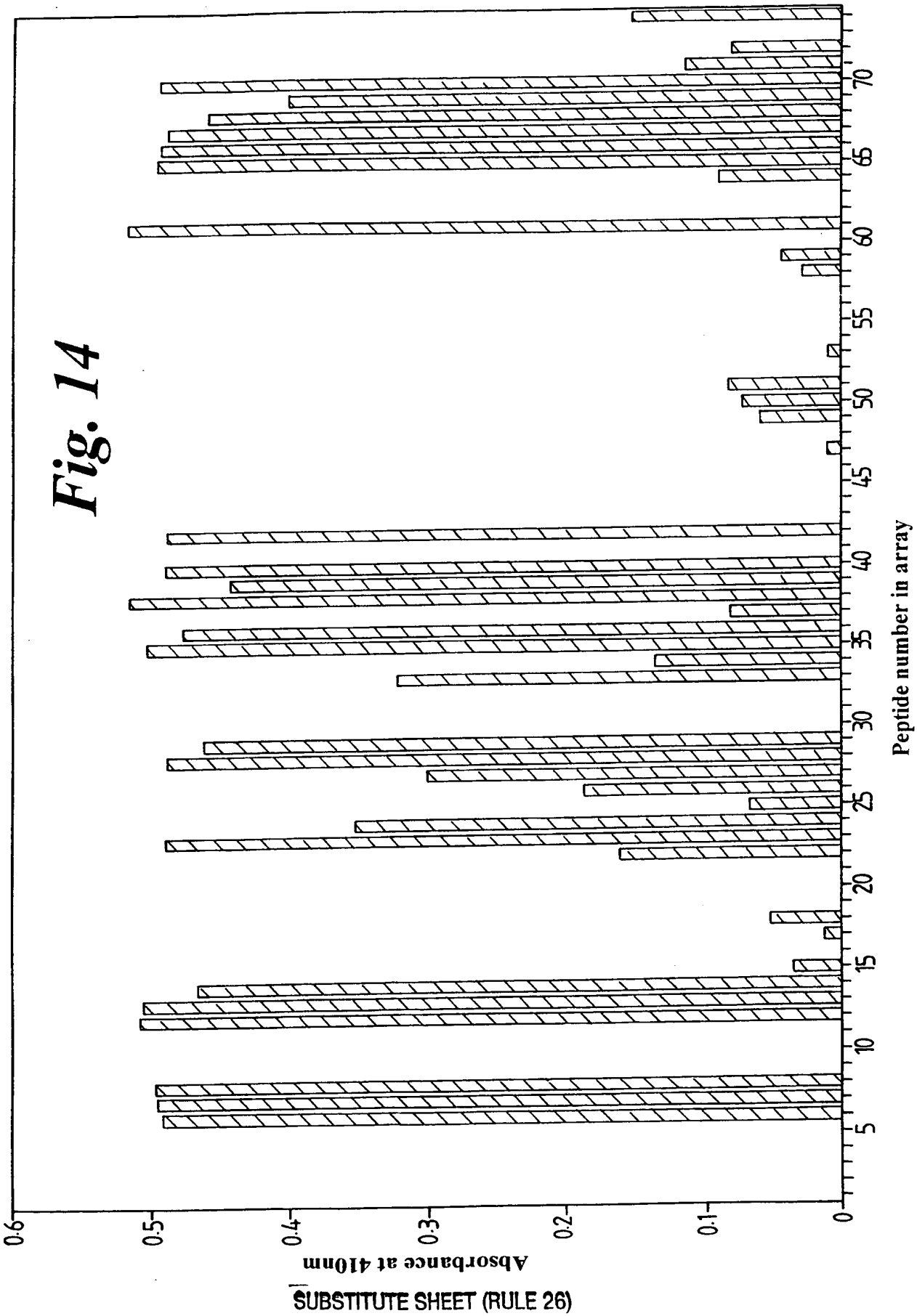


TABLE 2

mouse beta actin - 15mer peptides with 5 residue overlap

1,	MDDDIAALVVDNGSG	= 1 - 15
2,	AALVVDNGSGMCKAG	= 6 - 20
3,	DNGSGMCKAGFAGDD	= 11 - 25
4,	MCKAGFAGDDAPRAV	= 16 - 30
5,	FAGDDAPRAVFPSIV	= 21 - 35
6,	APRAVFPSIVGRPRH	= 26 - 40
7,	FPSIVGRPRHQGVMV	= 31 - 45
8,	GRPRHQGVMVGMGQK	= 36 - 50
9,	QGVMVGMGQKDSYVG	= 41 - 55
10,	GMGQKDSYVGDEAQS	= 46 - 60
11,	DSYVGDEAQSKRGIL	= 51 - 65
12,	DEAQSKRGILTLKYP	= 56 - 70
13,	KRGILTLKYPIEHGI	= 61 - 75
14,	TLKYPIEHGIVTNWD	= 66 - 80
15,	IEHGIVTNWDDMEKI	= 71 - 85
16,	VTNWDDMEKIWHHTF	= 76 - 90
17,	DMEKIWHHTFYNELR	= 81 - 95
18,	WHHTFYNELRVAPEE	= 86 - 100
19,	YNELRVAPEEHPVLL	= 91 - 105
20,	VAPEEHPVLLTEAPL	= 96 - 110
21,	HPVLLTEAPLNPKAN	= 101 - 115
22,	TEAPLNPKANREKMT	= 106 - 120
23,	NPKANREKMTQIMFE	= 111 - 125
24,	REKMTQIMFETFNTP	= 116 - 130
25,	QIMFETFNTPAMYVA	= 121 - 135
26,	TFNTPAMYVAIQAVL	= 126 - 140
27,	AMYVAIQAVLSLYAS	= 131 - 145
28,	IQAVLSLYASGRTTG	= 136 - 150
29,	SLYASGRTTGIVMDS	= 141 - 155
30,	GRTTGIVMDSGDGVT	= 146 - 160
31,	IVMDSGDGVTHTVPI	= 151 - 165
32,	GDGVTHTVPIYEGYA	= 156 - 170
33,	HTVPIYEGYALPHAI	= 161 - 175
34,	YEGYALPHAILRLDL	= 166 - 180
35,	LPHAILRLDLAGRDL	= 171 - 185
36,	LRLDLAGRDLTDYLM	= 176 - 190
37,	AGRDLTDYLMKILTE	= 181 - 195
38,	TDYLMKILTERGYSF	= 186 - 200
39,	KILTERGYSFTTTAE	= 191 - 205
40,	RGYSFTTTAEREIVR	= 196 - 210
41,	TTTAEREIVRDIKEK	= 201 - 215
42,	REIVRDIKEKLCYVA	= 206 - 220
43,	DIKEKLCYVALDFEQ	= 211 - 225
44,	LCYVALDFEQEMATA	= 216 - 230

45, LDFEQEMATAASSSS = 221 - 235
46, EMATAASSSSLEKSY = 226 - 240
47, ASSSSLEKSYELPDG = 231 - 245
48, LEKSYELPDGQVITI = 236 - 250
49, ELPDGQVITIGNERF = 241 - 255
50, QVITIGNERFRCPEA = 246 - 260
51, GNERFRCPEALFQPS = 251 - 265
52, RCPEALFQPSFLGME = 256 - 270
53, LFQPSFLGMESCGIH = 261 - 275
54, FLGMESCGIHETTFN = 266 - 280
55, SCGIHETTFNSIMKC = 271 - 285
56, ETTFNSIMKCDVDIR = 276 - 290
57, SIMKCDVDIRKDLYA = 281 - 295
58, DVDIRKDLYANTVLS = 286 - 300
59, KDLYANTVLSGGTTM = 291 - 305
60, NTVLSGGTTMYPGIA = 296 - 310
61, GGTTMYPGIADRMQK = 301 - 315
62, YPGIADRMQKEITAL = 306 - 320
63, DRMQKEITALAPSTM = 311 - 325
64, EITALAPSTMKIKII = 316 - 330
65, APSTMKIKIIAPPER = 321 - 335
66, KIKIIAPPERKYSVW = 326 - 340
67, APPERKYSVWIGGSI = 331 - 345
68, KYSVWIGGSILASLS = 336 - 350
69, IGGSILASLSTFQQM = 341 - 355
70, LASLSTFQQMWISKQ = 346 - 360
71, TFQQMWISKQEYDES = 351 - 365
72, WISKQEYDESGPSIV = 356 - 370
73, EYDESGPSIVHRKCF = 361 - 375
74, GGGGGGPSIVHRKCF = 366 - 375
75, GGGGGGGGGGHRKCF = 371 - 375

Other peptides to include:

76, KYSVWIGGSILASLS
alpha helix in subdomain 1 of rabbit alpha actin-contains two hydrophobic residues accessible to solvent
(residues S338 - S348)

77,PRHQGVMVGMGQKDS
loop in subdomain 2 of rabbit alpha actin-major interaction site with DNase I
(residues P38 - S52)

78, IVLDSGDGVTHNVPI
beta stands in subdomain 3 of rabbit alpha actin
(residues G150 - Y166)

79, LVCDNGSGLVKAGFA

analagous beta strand motif in subdomain 1 of rabbit alpha actin
(residues L8 - F21)

80, LFQPSFIGMESAGIH
loop in subdomain 4 of rabbit alpha actin-involved in contact across helix axis in F-actin
(residues F262 - L274)

81, TTAEREIVRDIKEKL
Alpha helix in subdomain 4 of rabbit alpha actin-minor interaction site with DNase I
(residues T203 - L216)

82, YVGDEAQSKRGILTL
beta alpha beta unit in subdomain 2 of rabbit alpha actin-minor interaction site with DNase I/ hexokinase-like unit
(residues K61 - L65)

83, VMSGGTTMYPGIADR
loop in subdomain 3 of rabbit alpha actin-forms pocket for adenine base of nucleotide
(residues S300 -I309)

84, KIKIIAPPERKYSVW
beta strand and loop in subdomain 3 of rabbit alpha actin-forms pocket for adenine base of nucleotide
(residues K328 - S338)

85, GFAGDDAPRAVFPSI
loop in subdomain 1 of rabbit alpha actin-central contact region of myosin on 'flat' side of actin
(residues F21 - P32)

86, YNELRVAPEEHPTLL
loop in subdomain 1 of rabbit alpha actin-contact region of myosin on 'flat' side of actin
(residues N92 - T103)

87, TFQQMWITKQEYDEA
alpha helices in subdomain 1 of rabbit alpha actin-bind myosin chains
(residues S348 - A365)

88, DEDETTALVCDNGSG
N-terminal 15 residues of rabbit alpha actin-important in binding myosin
(residues D1 - G15)

89, EYDEAGPSIVHRKCF
C-terminal 15 residues of rabbit alpha actin
(residues E361 - F375)

90, SKQEYDESGPSIVHR
truncated C-terminus of mouse beta actin
(reidues S358 - R372)

91, ILTERGYSFVTTAER
loop in subdomain 4 of rabbit alpha actin-analagous to DNase I-binding loop in subdomain 2
(residues T194 - T203)

92, ALDFENEMATAASSS
alpha helix flanked by loops in subdomain 4 of rabbit alpha actin
(residues F223 - A230)

93, WDDMEKIWHHTFYNE
alpha helix in subdomain 1 of rabbit alpha actin
(residues W79 - N92)

94, +ve control for 91a = STDLVAKLRAFHNEA